

FIG. 1

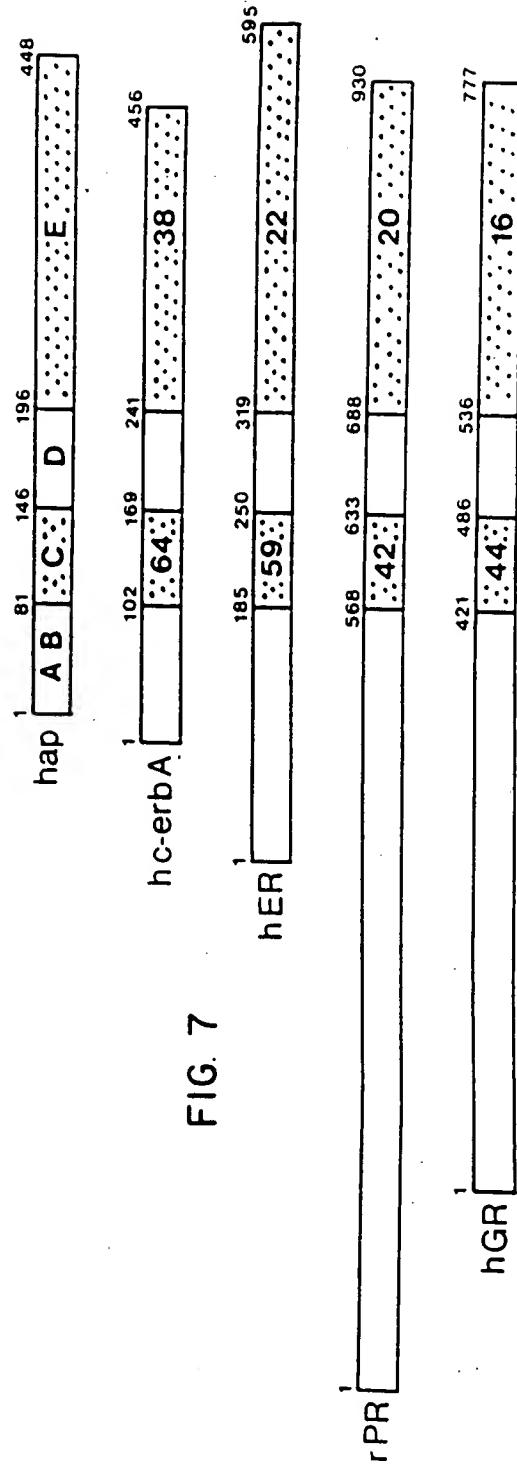


FIG. 7

CGGGGTAGGATCCGAACCCATCGAACGGCTTTGCAAGCATTACTGGAACGGAACTTGGATCTTCTG 75
 CGAACCCCCCCCCGGCTGGATTGGCCGAGCAAGGCCCTGGAAATGCTAAATGATCATTTGATCAATTACAGG 150
 TTTTACCTGGCTTGTCTCTCATATTATGATCTGGGGCTGGAAAAAGACCAACAGGCCAACGGCTACGTGCCAAAAAAGG 225
 CGCAGAGTTGATGGAGTTGGGACTTTCTATCCCATTTGCTCCACACCTAGACGGATAAGCACTTTGCAG 300
1 10
 HetPheAspCysNetAspValLeuSerValSerProGlyGinIleLeuAspPhe 375
 ACATTCACTGCAAGGAGATCATCTTGTACTGTATGGATTTCTGACTGACTCCTGGCCAAATCTGGATTTC 40
 20 30 40
 TyrThrAlaSerProSerSerCysLeuGluLysAlaLeuLysAlaCysPheSerGlyLeuThrGluThr 450
 TAGACTGGAGTCCGCTTCCCTGCTCCACAGAGAACCTCTAAACCATGCTTCACTGATTGACCCAAACC 50 60
 GluTrpGlnHisArgHisThrAlaGlnSerIleGluThrGlnSerThrSerGluGluLeuValProSerPro 525
 GAATGCCAGCATGGCACACTGCTCAATTGAAACACAGACCCAGCTCTGAGGAACCTCCAAAGCCC 70 80 90
 ProSerProLeuProProProArgValTyrLysProCysPheValCysGlnAspLysSerSerGlyTyrHisTyr 600
 CCATCTCCACTTCTCCCCCTGAGCTACAAACCTGCTTCCGAGCACAAATCATCAGGGTACCAACTAT 100 110
 GlyValSerAlaCysGluGlyCysLysGlyPheArgArgSerIleGlnAspMetIleTyrThrCysHis 675
 GGGGTCAGCCCTGAGGGATGTAACGGCTTTCCCGAGAAGTATTCAAGAAATAATGATTACACTTCTCAC 120 130 140
 ArgAspLysAsnCysValIleAsnLysValThrArgAsnArgCysGlnTyrCysArgLeuGlnLysCysPheGlu 750
 CGAGATTAAGAACCTGTTTAAATAAACTCACCAGGAATGCAAACTGCAACTTGTCCACTCCAGAACGCTTC 150 160
 ValGlyHetSerLysGluSerValArgAsnAspArgAsnLysLysGluThrSerLysGlnGluCysThr 825
 GTGGGAATGTCCAAGAACATCTGCAAGGATGACAGGAACAAAGAAAAAGAAGGAGACTTCAAAAGAACATGCACA 170 180 190
 GluSerTyrGluHetThrAlaGluLeuAspLeuThrGluLysIleArgLysAlaHisGlnGluThrPhePro 900
 GAGACCTATGAAATGACAGCTGCTGGAGCATCTGACAGAGAGATCCGAAAAGCTCACCCAGAACACTTCCCT 200 210
 SerLeuCysGluLeuGlyLysTyrThrThrAsnSerSerAlaAspHisArgValArgLeuAspLeuGlyLeuTrp 975
 TCACTCTGCCAGCTGGCTAAATACACCACGATTCCACTGCTGACCCTGGACTCCGACTGGCCCTCTGG 220 230 240
 AspLysPheSerGluLeuAlaThrLysCysIleLeuValGluPheAlaLysArgLeuProGlyPheThr 1050
 GACAAATTCAGTCAACTGCCACCAAGTCCATTAAAGATCTGGACTTGTCTAAACCTCTGGCTTTC 250 260
 GlyLeuThrIleAlaAspGlnIleThrLeuLeuLysAlaAlaCysLeuAspIleLeuLeuArgLysThr 1125
 GGCTTGACCATGGCAGACCAAATTACCCCTGCTGAGGGCCCTGCCCTGGACATCCTGATTCATTAACTTCCACC 270 280 290
 ArgTyrThrProGluGlnAspThrHetThrPheSerAspGlyLeuThrLeuAsnArgThrGlnHetHisAsnAla 1200
 AGCTATACCCCAGAACAGACCCATCACTTCTCACAGCGCCITACCTTAACTGAACTCAGATCCAAATGCT 300 310
 GlyPheGlyProLeuThrAspLeuValPheThrPheAlaAsnGlnLeuLeuProLeuGluMetAspAspThrGlu 1275
 GGATTGGTCTCTGACTGACCTTGCTTCACTTGGCAACCACCTCTGGAAATGGATGACACAGAA 320 330 340
 ThrIleLeuLeuSerAlaIleCysLeuIleCysGlyAspArgGlnAspLeuGluGluProThrLysValAspLys 1350
 ACAGCCCTTCTGACTGCCATCTGCTTAACTGIGAGACGGCCAGGACCTTGAGGAACCCGACAAAAGTAGATAAG 350 360
 LeuGlnGluProLeuLeuGluAlaLeuLysIleTyrIleArgLysArgArgProSerLysProHisNetPhePro 1425
 CTACAAGAACCATGGAGGACTAAATTTATATCAGAAAAAGACGACCCAGCAAGCCTCACATGTTTCCA 370 380 390
 LysIleLeuHetLysIleThrAspLeuArgSerIleSerAlaLysGlyAlaGluArgValIleThrLeuLysIle 1500
 AGATCTTAATGAAATCAGATCTCCCTACCATGCTAAAGCTCAGAGGGCTTAATTACCTGAAATG 400 410
 GluIleProGlySerMetProLeuIleGlnGluHetMetGluAsnSerGluGlyHisGluProLeuThrPro 1575
 GAAATCTGATCAATGCCACCTCTCATTAAGAAATGATGGAGAATTCTGAAGGACATGAACCCCTGACCCCA 420 430 440
 SerSerSerGlyAsnThrAlaGluHisSerProSerIleSerProSerSerValGluAsnSerGlyValSerGln 1650
 ACTTCAAGTGGAACACAGGACAGCTAGCATCTACCCAGCTAGCTACGAAACTGCTCAGTGGAAAACACTGGCTCAGTCAG
 SerProLeuValGlnSTOP
 TCACCACTCTGCAATACACATTCTAGTACTTCACCAACATTCCCGACTACCTTCAGTTCCAGGATTTAAAT 1725
 GCAAGAAAAAACATTTTACTGCTGCTTACATTTCGACTGAAAGATTTAAACCTCAAGAACGGACCAAGACT 1800
 TTTCATATGATCAATATATATACCTCTCATGCTTACCTTACCTACGAAATTTAAACCTCAAGAACGGACCAAGACT 1875
 TGACCCCAATTGATGCAAGGACCAAGAACCTGTTAAAGCTCTTACCTACGAAATTTAAACCTCAAGATGCTGGCAAA 1950
 GACCCCACTAAATGATTTACCCCTGCTTAACTTTCTGCTGCTGCTACATCAAGAACGGACTATGGCTCTGTT 2025
 CTATACGCTATGTTGGTGTCTCTGCTGCTGCTACATCAAGAACGGACTATGGCTCTGTT 2100
 CTACTGTACCGTCTACCTACGGTCAAAAGATAACTCTGCTTTCATGGAATAGCTCAAGAACATCAAGCTAAG 2175
 GAAAACAGGACTATTGACAGGACTATGTCAGTACGACAGATAAGGCTGAAGGATATTCTACTTACTGATG 2250
 GAAGCTTGCTTTCGCTTCTGATGCTCAACTGCTCAACTGCTTACGTTCTGCTTACGCTTACGCTTACGCTTACG 2325
 TTCCCTGCACTAGCAGAACGAAATTCTGATCATGCTTACGCTGACTGCTGCTTACGCTTACGCTTACGCTTACG 2400
 TGTTAAATGTCATTTAAATGAGCTTAAACTCTGCTTAACTGACATAACTACAGCTGCTTACGCTTACGCTTACG 2475
 TTTTTCAGTAATGATGCGCTCAAGGCAAGAACACTTCTGCTGCTTACCCACTGACCATGTAACCTCTGCTCTG 2550
 ATTACGGAAATTCTGATGGATAATTAGCAGGCTGCTTACCCACTGACCATGTAACCTCTGCTCTGCTCTG 2625
 CATGCTGATATTGGGATTTTCCACCCCTCTGATGCCAACGGCTTAATTATACATCCCAAGGAAACAG 2700
 GCATAGAACATGGCTCTTACCTGCTCAACTGACAGAACGGCTGACAGTCAAGGCTGCTGAGTGGTAAACAG 2775
 ATACAAGCTGAGTTCTTACTCTCATTAAGCAGTACGCTGCAATTCTTCTGATATATTAGCAGACTGCTG 2850
 ATGACTTTACTGGCTCTGTTGATCATGAGATTGTTCTTAAACATGCTTCTGATATACTGTT 2925
 CTTTTCCATGGAGTCTGCTGCCAAAGATAAAATATATTATTTAAATTTAAAAA 2992

FIG. 2

FIG. 3

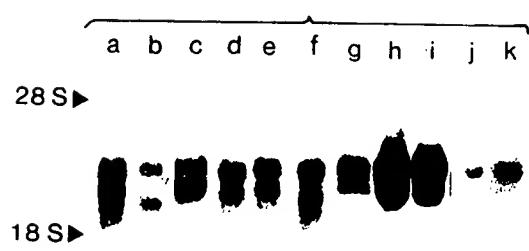


FIG. 4

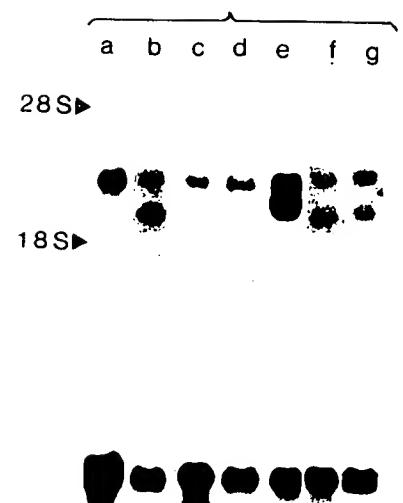


FIG. 6

FIG. 8A

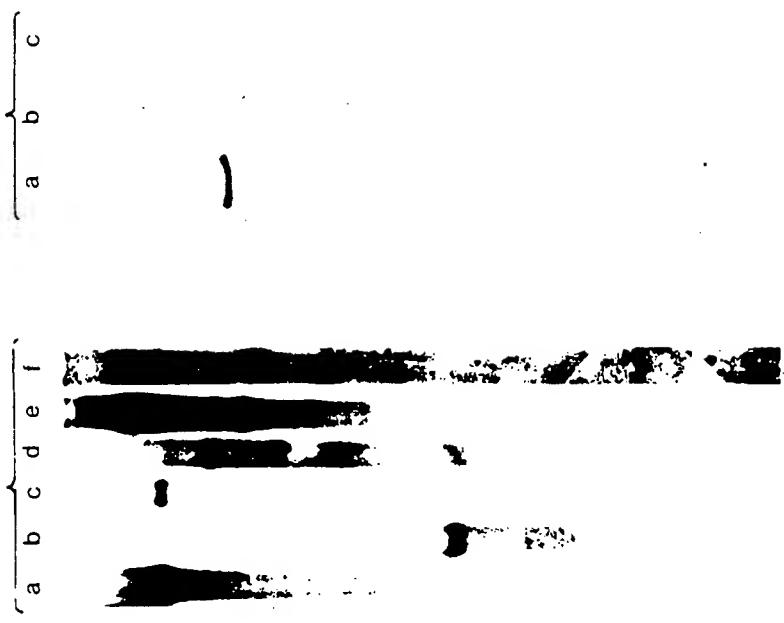


FIG. 8B

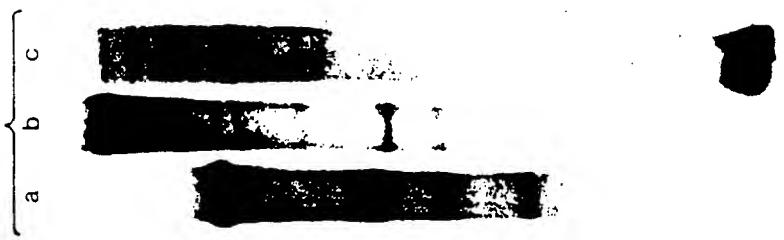
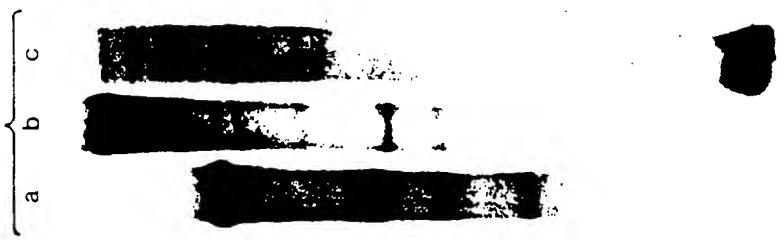


FIG. 8C



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FIG. 15

5' END

FIG. 16



FIG. 11

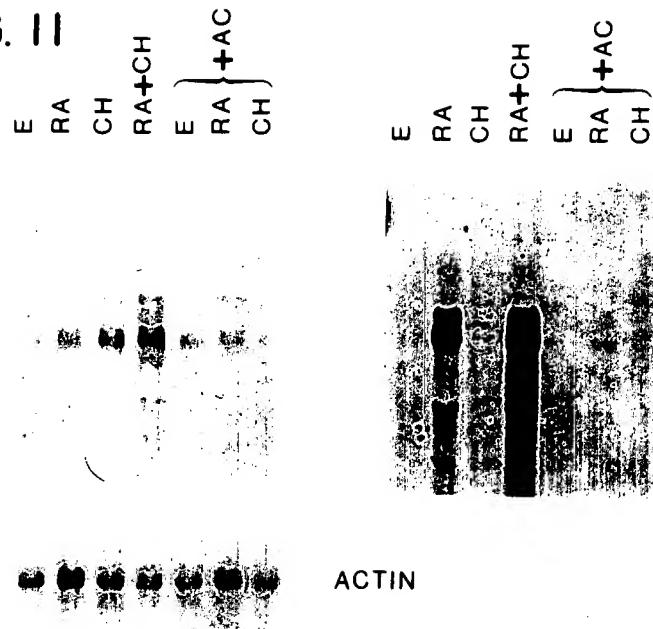


FIG. 14

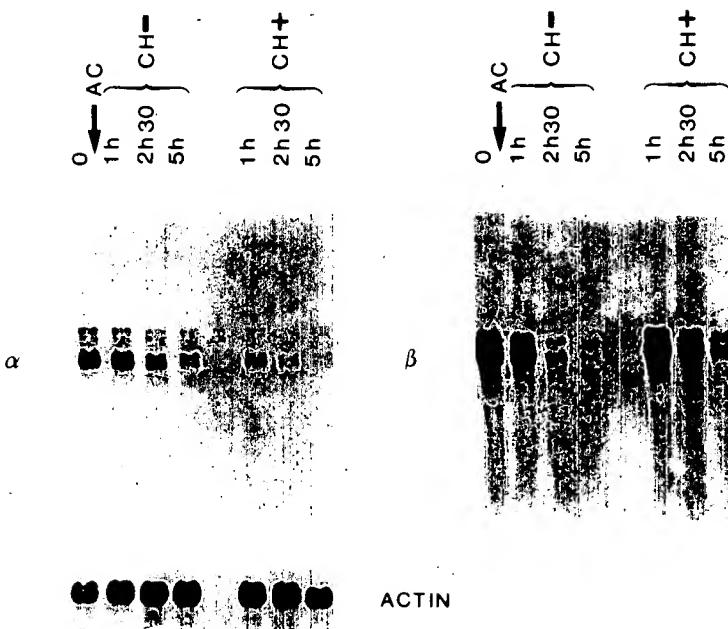


FIG. 9

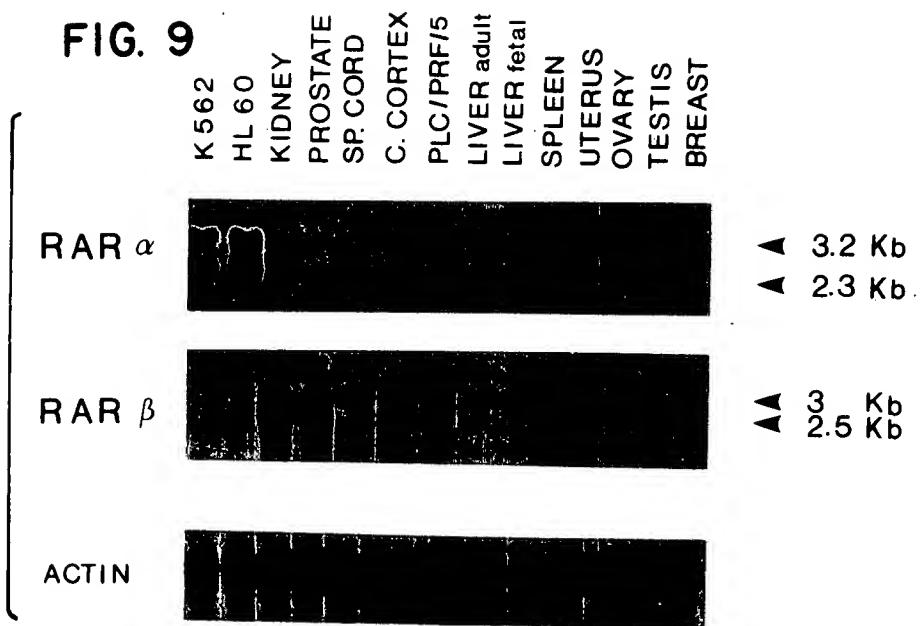
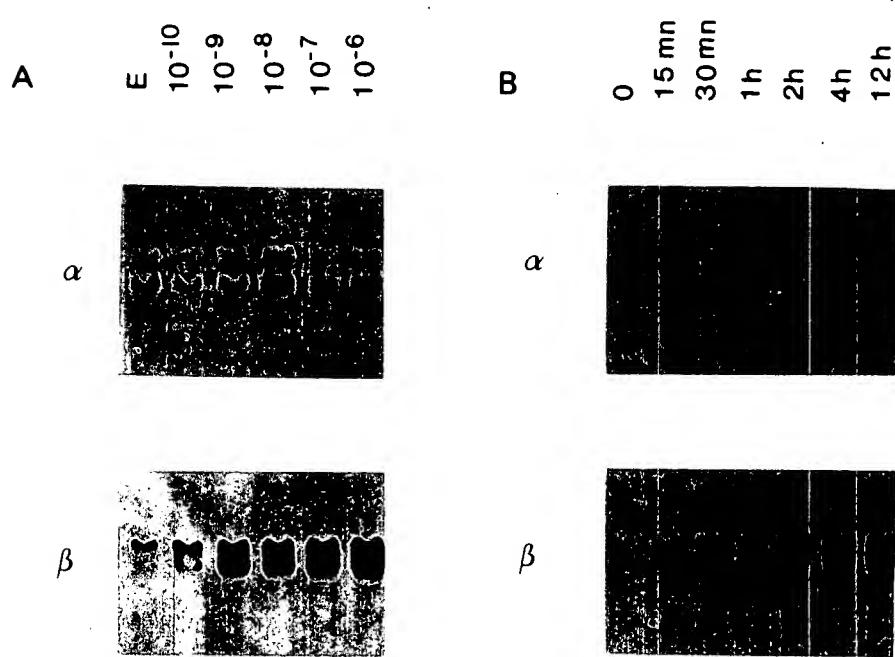


FIG. 10



a b c

M_r
(K)

- 97
- 68
- 43
- 26

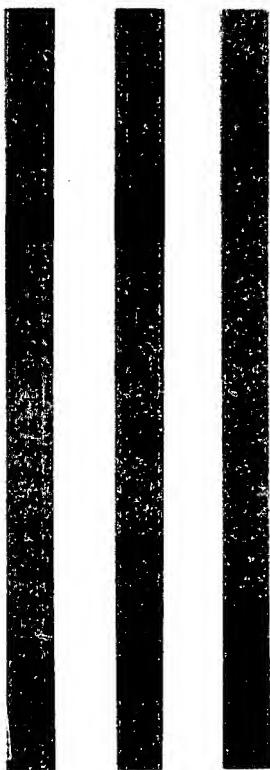


FIG. 12

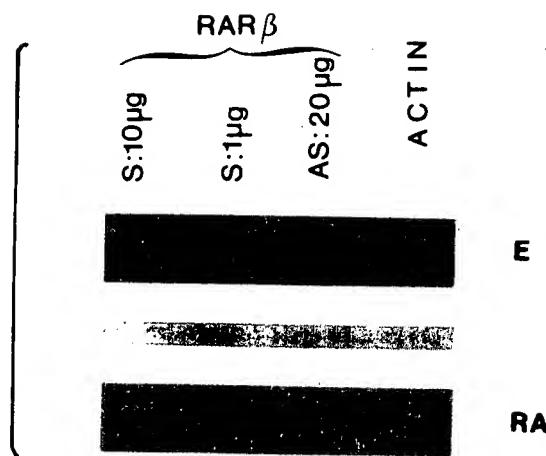


FIG. 13

